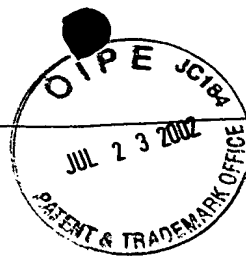


#6

SEQUENCE LISTING



<110> Hobbs, Helen H.
 Shan, Bei
 Barnes, Robert
 Tian, Hui
 Tularik Inc.
 Board of Regents, The University of Texas System

<120> ABCG5 and ABCG8: Compositions and Methods of Use

<130> 018781-007320US

<140> US 09/989,981

<141> 2001-11-20

<150> US 60/252,235

<151> 2000-11-20

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Thr Glu Ala Arg His Ser Leu Gly Val Leu His Val Ser Tyr Ser Val	
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Trp Asp Arg Gln Ile Leu Lys Asp Val Ser Leu Tyr Ile Glu Ser Gly	
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Gln Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu	
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 Ser Ala Asp Phe Tyr Asn Lys Lys Val Glu Ala Val Met Thr Glu Leu
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 225 230 235 240

cgc agg gac cga att gtg att gtc acc atc cac cag cct cgc tct gag 768
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Thr Ser Met Leu Asn His Pro Met Cys Ala Ile Thr Gln Gly Val Gln
595 600 605

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Gln Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu
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Gly Ile Ser Ser Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu
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225 230 235 240

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 Val Ile Phe Ser Ser Val Cys Tyr Trp Thr Leu Gly Leu Tyr Pro Glu
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 Asn Ile Val Asn Ser Ile Val Ala Leu Leu Ser Ile Ser Gly Leu Leu
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 Ile Gly Ser Gly Phe Ile Arg Asn Ile Gln Glu Met Pro Ile Pro Leu
 545 550 555 560
 Lys Ile Leu Gly Tyr Phe Thr Phe Gln Lys Tyr Cys Cys Glu Ile Leu
 565 570 575
 Val Val Asn Glu Phe Tyr Gly Leu Asn Phe Thr Cys Gly Gly Ser Asn
 580 585 590
 Thr Ser Met Leu Asn His Pro Met Cys Ala Ile Thr Gln Gly Val Gln
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 Asp Asn Ser Leu Tyr Phe Thr Tyr Ser Gly Gln Ser Asn Thr Leu Glu
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gtc aga gat ctc acc tac cag gtg gac atc gcc tct cag gtg cct tgg 192
 Val Arg Asp Leu Thr Tyr Gln Val Asp Ile Ala Ser Gln Val Pro Trp
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 Phe Glu Gln Leu Ala Gln Phe Lys Ile Pro Trp Arg Ser His Ser Ser
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caa gac tcc tgt gag ctg ggc atc cga aat cta agc ttc aaa gtg agg 288
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agt gga cag atg ctg gcc atc ata ggg agc tca ggc tgc ggg aga gcc 336
 Ser Gly Gln Met Leu Ala Ile Ile Gly Ser Ser Gly Cys Gly Arg Ala
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 Ser Leu Leu Asp Val Ile Thr Gly Arg Gly His Gly Gly Lys Met Lys
 115 120 125

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 130 135 140

agg aag tgc gtt gcg cat gtg cgg cag cat gac caa ctg ctg ccc aac 480
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 Ala Glu Leu Arg Leu Arg Gln Cys Ala Asn Thr Arg Val Gly Asn Thr
 195 200 205

tat gta cgt ggg gtg tcc ggg ggt gag cgc cga cga gtg agc att ggg 672
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 210 215 220

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Arg Leu Ala Lys Gly Asn Arg Leu Val Leu Ile Ser Leu His Gln Pro	
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Gly Thr Pro Ile Tyr Leu Gly Ala Ala Gln Gln Met Val Gln Tyr Phe	
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Thr Ser Ile Gly His Pro Cys Pro Arg Tyr Ser Asn Pro Ala Asp Phe	
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Tyr Val Asp Leu Thr Ser Ile Asp Arg Arg Ser Lys Glu Arg Glu Val	
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gcc acc gtg gag aag gca cag tct ctt gca gcc ctg ttc cta gaa aaa	1056
Ala Thr Val Glu Lys Ala Gln Ser Leu Ala Ala Leu Phe Leu Glu Lys	
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Cys Gly Thr Ala Val Glu Leu Pro Gly Met Ile Glu Gln Phe Ser Thr	
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Ala Leu Ala Ala Ser Ala Met Leu Pro Thr Phe His Met Ser Ser Phe
545 550 555 560

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625 630 635 640

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645 650 655

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Ser Gly Gln Ile Trp Ile Asn Gly Gln Pro Ser Thr Pro Gln Leu Val
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 ggggtccggcc accagaaaat ttgcccagct ttgctgcctg ttggcc atg ggt gac 115
 Met Gly Asp
 1
 ctc tca tct ttg acc ccc gga ggg tcc atg ggt ctc caa gta aac aga 163
 Leu Ser Ser Leu Thr Pro Gly Gly Ser Met Gly Leu Gln Val Asn Arg
 5 10 15
 ggc tcc cag agc tcc ctg gag ggg gct cct gcc acc gcc ccg gag cct 211
 Gly Ser Gln Ser Ser Leu Glu Gly Ala Pro Ala Thr Ala Pro Glu Pro
 20 25 30 35
 cac agc ctg ggc atc ctc cat gcc tcc tac agc gtc agc cac cgc gtg 259
 His Ser Leu Gly Ile Leu His Ala Ser Tyr Ser Val Ser His Arg Val
 40 45 50

agg cec tgg tgg gac atc aca tct tgc cgg cag cag tgg acc agg cag 307
 Arg Pro Trp Trp Asp Ile Thr Ser Cys Arg Gln Gln Trp Thr Arg Gln
 55 60 65

atc ctc aaa gat gtc tcc ttg tac gtg gag agc ggg cag atc atg tgc 355
 Ile Leu Lys Asp Val Ser Leu Tyr Val Glu Ser Gly Gln Ile Met Cys
 70 75 80

atc cta gga agc tca ggc tcc ggg aaa acc acg ctg ctg gac gcc atg 403
 Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu Leu Asp Ala Met
 85 90 95

tcc ggg agg ctg ggg cgc gcg ggg acc ttc ctg ggg gag gtg tat gtg 451
 Ser Gly Arg Leu Gly Arg Ala Gly Thr Phe Leu Gly Glu Val Tyr Val
 100 105 110 115

aac ggc cgg gcg ctg cgc cgg gag cag ttc cag gac tgc ttc tcc tac 499
 Asn Gly Arg Ala Leu Arg Arg Glu Gln Phe Gln Asp Cys Phe Ser Tyr
 120 125 130

gtc ctg cag agc gac acc ctg ctg agc agc ctc acc gtg cgc gag acg 547
 Val Leu Gln Ser Asp Thr Leu Leu Ser Ser Leu Thr Val Arg Glu Thr
 135 140 145

ctg cac tac acc gcg ctg ctg gcc atc cgc cgc ggc aat ccc ggc tcc 595
 Leu His Tyr Thr Ala Leu Leu Ala Ile Arg Arg Gly Asn Pro Gly Ser
 150 155 160

ttc cag aag aag gtg gag gcc gtc atg gca gag ctg agt ctg agc cat 643
 Phe Gln Lys Lys Val Glu Ala Val Met Ala Glu Leu Ser Leu Ser His
 165 170 175

gtg gca gac cga ctg att ggc aac tac agc ttg ggg ggc att tcc acg 691
 Val Ala Asp Arg Leu Ile Gly Asn Tyr Ser Leu Gly Gly Ile Ser Thr
 180 185 190 195

ggt gag cgg cgc cgg gtc tcc atc gca gcc cag ctg ctc cag gat cct 739
 Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu Leu Gln Asp Pro
 200 205 210

aag gtc atg ctg ttt gat gag cca acc aca ggc ctg gac tgc atg act 787
 Lys Val Met Leu Phe Asp Glu Pro Thr Thr Gly Leu Asp Cys Met Thr
 215 220 225

gct aat cag att gtc gtc ctc ctg gtg gaa ctg gct cgc agg aac cga 835
 Ala Asn Gln Ile Val Val Leu Leu Val Glu Leu Ala Arg Arg Asn Arg
 230 235 240

att gtg gtt ctc acc att cac cag ccc cgt tct gag ctt ttt cag ctc 883
 Ile Val Val Leu Thr Ile His Gln Pro Arg Ser Glu Leu Phe Gln Leu
 245 250 255

ttt gac aaa att gcc atc ctg agc ttc gga gag ctg att ttc tgt ggc 931
 Phe Asp Lys Ile Ala Ile Leu Ser Phe Gly Glu Leu Ile Phe Cys Gly
 260 265 270 275

acg cca gcg gaa atg ctt gat ttc ttc aat gac tgc ggt tac cct tgt 979
 Thr Pro Ala Glu Met Leu Asp Phe Phe Asn Asp Cys Gly Tyr Pro Cys
 280 285 290

cct gaa cat tca aac cct ttt gac ttc tat atg gac ctg acg tca gtg 1027
 Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp Leu Thr Ser Val
 295 300 305

gat acc caa agc aag gaa cgg gaa ata gaa acc tcc aag aga gtc cag 1075
 Asp Thr Gln Ser Lys Glu Arg Glu Ile Glu Thr Ser Lys Arg Val Gln
 310 315 320

atg ata gaa tct gcc tac aag aaa tca gca att tgt cat aaa act ttg 1123
 Met Ile Glu Ser Ala Tyr Lys Lys Ser Ala Ile Cys His Lys Thr Leu
 325 330 335

aag aat att gaa aga atg aaa cac ctg aaa acg tta cca atg gtt cct 1171
 Lys Asn Ile Glu Arg Met Lys His Leu Lys Thr Leu Pro Met Val Pro
 340 345 350 355

ttc aaa acc aaa gat tct cct gga gtt ttc tct aaa ctg ggt gtt ctc 1219
 Phe Lys Thr Lys Asp Ser Pro Gly Val Phe Ser Lys Leu Gly Val Leu
 360 365 370

ctg agg aga gtg aca aga aac ttg gtg aga aat aag ctg gca gtg att 1267
 Leu Arg Arg Val Thr Arg Asn Leu Val Arg Asn Lys Leu Ala Val Ile
 375 380 385

acg cgt ctc ctt cag aat ctg atc atg ggt ttg ttc ctc ctt ttc ttc 1315
 Thr Arg Leu Leu Gln Asn Leu Ile Met Gly Leu Phe Leu Leu Phe Phe
 390 395 400

gtt ctg cgg gtc cga agc aat gtg cta aag ggt gct atc cag gac cgc 1363
 Val Leu Arg Val Arg Ser Asn Val Leu Lys Gly Ala Ile Gln Asp Arg
 405 410 415

gta ggt ctc ctt tac cag ttt gtg ggc gcc acc ccg tac aca ggc atg 1411
 Val Gly Leu Leu Tyr Gln Phe Val Gly Ala Thr Pro Tyr Thr Gly Met
 420 425 430 435

ctg aac gct gtg aat ctg ttt ccc gtg ctg cga gct gtc agc gac cag 1459
 Leu Asn Ala Val Asn Leu Phe Pro Val Leu Arg Ala Val Ser Asp Gln
 440 445 450

gag agt cag gac ggc ctc tac cag aag tgg cag atg atg ctg gcc tat 1507
 Glu Ser Gln Asp Gly Leu Tyr Gln Lys Trp Gln Met Met Leu Ala Tyr
 455 460 465

gca ctg cac gtc ctc ccc ttc agc gtt gtt gcc acc atg att ttc agc 1555
 Ala Leu His Val Leu Pro Phe Ser Val Val Ala Thr Met Ile Phe Ser
 470 475 480

agt gtg tgc tac tgg acg ctg ggc tta cat cct gag gtt gcc cga ttt 1603
 Ser Val Cys Tyr Trp Thr Leu Gly Leu His Pro Glu Val Ala Arg Phe
 485 490 495

gga tat ttt tct gct gct ctc ttg gcc ccc cac tta att ggt gaa ttt 1651
 Gly Tyr Phe Ser Ala Ala Leu Leu Ala Pro His Leu Ile Gly Glu Phe
 500 505 510 515

cta act ctt gtg cta ctt ggt atc gtc caa aat cca aat ata gtc aac 1699
 Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro Asn Ile Val Asn
 520 525 530

agt gta gtg gct ctg ctg tcc att gcg ggg gtg ctt gtt gga tct gga 1747
 Ser Val Val Ala Leu Leu Ser Ile Ala Gly Val Leu Val Gly Ser Gly
 535 540 545

ttc ctc aga aac ata caa gaa atg ccc att cct ttt aaa atc atc agt 1795
 Phe Leu Arg Asn Ile Gln Glu Met Pro Ile Pro Phe Lys Ile Ile Ser
 550 555 560

tat ttt aca ttc caa aaa tat tgc agt gag att ctt gta gtc aat gag 1843
 Tyr Phe Thr Phe Gln Lys Tyr Cys Ser Glu Ile Leu Val Val Asn Glu
 565 570 575

ttc tac gga ctg aat ttc act tgt ggc agc tca aat gtt tct gtg aca 1891
 Phe Tyr Gly Leu Asn Phe Thr Cys Gly Ser Ser Asn Val Ser Val Thr
 580 585 590 595

act aat cca atg tgt gcc ttc act caa gga att caa ttc att gag aaa 1939
 Thr Asn Pro Met Cys Ala Phe Thr Gln Gly Ile Gln Phe Ile Glu Lys
 600 605 610

acc tgc cca ggt gca aca tct aga ttc aca atg aac ttt ctg att ttg 1987
 Thr Cys Pro Gly Ala Thr Ser Arg Phe Thr Met Asn Phe Leu Ile Leu
 615 620 625

tat tca ttt att cca gct ctt gtc atc cta gga ata gtt gtt ttc aaa 2035
 Tyr Ser Phe Ile Pro Ala Leu Val Ile Leu Gly Ile Val Val Phe Lys
 630 635 640

ata agg gat cat ctc att agc agg tag tgaaagccat ggctgggaaa 2082
 Ile Arg Asp His Leu Ile Ser Arg
 645 650

atggaagtga agctgccgac tgtgcatgac tgctctgaac gtctgaaatg agagtgccat 2142

gtattttcttt cttgacagga catctcaagt cttttaacca ttaagactcc atttgtgcct 2202

cttgatcca agcaggcctt gaatgcaatg gaagtgggtt atagtccctt gctcttacia 2262

cttgcaggga catgtgggta tttggaaatt gtgactgagc ggacccaaga atgtaaataa 2322

tattcataaa cctatggg 2340

<210> 6
 <211> 651
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human ABCG5 (hABCG5)

<400> 6
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 Val Asn Arg Gly Ser Gln Ser Ser Leu Glu Gly Ala Pro Ala Thr Ala
 20 25 30
 Pro Glu Pro His Ser Leu Gly Ile Leu His Ala Ser Tyr Ser Val Ser
 35 40 45
 His Arg Val Arg Pro Trp Trp Asp Ile Thr Ser Cys Arg Gln Gln Trp
 50 55 60

Thr Arg Gln Ile Leu Lys Asp Val Ser Leu Tyr Val Glu Ser Gly Gln
 65 70 75 80
 Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu Leu
 85 90 95
 Asp Ala Met Ser Gly Arg Leu Gly Arg Ala Gly Thr Phe Leu Gly Glu
 100 105 110
 Val Tyr Val Asn Gly Arg Ala Leu Arg Arg Glu Gln Phe Gln Asp Cys
 115 120 125
 Phe Ser Tyr Val Leu Gln Ser Asp Thr Leu Leu Ser Ser Leu Thr Val
 130 135 140
 Arg Glu Thr Leu His Tyr Thr Ala Leu Leu Ala Ile Arg Arg Gly Asn
 145 150 155 160
 Pro Gly Ser Phe Gln Lys Lys Val Glu Ala Val Met Ala Glu Leu Ser
 165 170 175
 Leu Ser His Val Ala Asp Arg Leu Ile Gly Asn Tyr Ser Leu Gly Gly
 180 185 190
 Ile Ser Thr Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu Leu
 195 200 205
 Gln Asp Pro Lys Val Met Leu Phe Asp Glu Pro Thr Thr Gly Leu Asp
 210 215 220
 Cys Met Thr Ala Asn Gln Ile Val Val Leu Leu Val Glu Leu Ala Arg
 225 230 235 240
 Arg Asn Arg Ile Val Val Leu Thr Ile His Gln Pro Arg Ser Glu Leu
 245 250 255
 Phe Gln Leu Phe Asp Lys Ile Ala Ile Leu Ser Phe Gly Glu Leu Ile
 260 265 270
 Phe Cys Gly Thr Pro Ala Glu Met Leu Asp Phe Phe Asn Asp Cys Gly
 275 280 285
 Tyr Pro Cys Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp Leu
 290 295 300
 Thr Ser Val Asp Thr Gln Ser Lys Glu Arg Glu Ile Glu Thr Ser Lys
 305 310 315 320
 Arg Val Gln Met Ile Glu Ser Ala Tyr Lys Lys Ser Ala Ile Cys His
 325 330 335
 Lys Thr Leu Lys Asn Ile Glu Arg Met Lys His Leu Lys Thr Leu Pro
 340 345 350
 Met Val Pro Phe Lys Thr Lys Asp Ser Pro Gly Val Phe Ser Lys Leu
 355 360 365
 Gly Val Leu Leu Arg Arg Val Thr Arg Asn Leu Val Arg Asn Lys Leu
 370 375 380
 Ala Val Ile Thr Arg Leu Leu Gln Asn Leu Ile Met Gly Leu Phe Leu
 385 390 395 400
 Leu Phe Phe Val Leu Arg Val Arg Ser Asn Val Leu Lys Gly Ala Ile
 405 410 415
 Gln Asp Arg Val Gly Leu Leu Tyr Gln Phe Val Gly Ala Thr Pro Tyr
 420 425 430
 Thr Gly Met Leu Asn Ala Val Asn Leu Phe Pro Val Leu Arg Ala Val
 435 440 445
 Ser Asp Gln Glu Ser Gln Asp Gly Leu Tyr Gln Lys Trp Gln Met Met
 450 455 460
 Leu Ala Tyr Ala Leu His Val Leu Pro Phe Ser Val Val Ala Thr Met
 465 470 475 480
 Ile Phe Ser Ser Val Cys Tyr Trp Thr Leu Gly Leu His Pro Glu Val
 485 490 495
 Ala Arg Phe Gly Tyr Phe Ser Ala Ala Leu Leu Ala Pro His Leu Ile
 500 505 510
 Gly Glu Phe Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro Asn
 515 520 525
 Ile Val Asn Ser Val Val Ala Leu Leu Ser Ile Ala Gly Val Leu Val
 530 535 540

atc act ggc cga ggt cac ggc ggc aag atc aag tca ggc cag atc tgg 498
 Ile Thr Gly Arg Gly His Gly Gly Lys Ile Lys Ser Gly Gln Ile Trp
 120 125 130

atc aat ggg cag ccc agc tcg cct cag ctg gtg agg aag tgt gtg gcc 546
 Ile Asn Gly Gln Pro Ser Ser Pro Gln Leu Val Arg Lys Cys Val Ala
 135 140 145

cac gtg cgc cag cac aac cag ctg ctc ccc aac ttg act gtg cga gag 594
 His Val Arg Gln His Asn Gln Leu Leu Pro Asn Leu Thr Val Arg Glu
 150 155 160 165

acc ttg gcc ttc att gcc cag atg cgg ctg ccc aga acc ttc tcc cag 642
 Thr Leu Ala Phe Ile Ala Gln Met Arg Leu Pro Arg Thr Phe Ser Gln
 170 175 180

gcc cag cgt gac aaa agg gtg gag gac gtg atc gcg gag ctg cgg ctt 690
 Ala Gln Arg Asp Lys Arg Val Glu Asp Val Ile Ala Glu Leu Arg Leu
 185 190 195

agg cag tgc gct gac acc cgc gtg ggc aac atg tac gtg cgg ggg ttg 738
 Arg Gln Cys Ala Asp Thr Arg Val Gly Asn Met Tyr Val Arg Gly Leu
 200 205 210

tcg ggg ggt gag cgc agg aga gtc agc att ggg gtg cag ctc ctg tgg 786
 Ser Gly Gly Glu Arg Arg Arg Val Ser Ile Gly Val Gln Leu Leu Trp
 215 220 225

aac cca gga atc ctt att ctc gac gaa ccc acc tct ggg ctc gac agc 834
 Asn Pro Gly Ile Leu Ile Leu Asp Glu Pro Thr Ser Gly Leu Asp Ser
 230 235 240 245

ttc aca gcc cac aac ctg gtg aag acc ttg tcc agg ctg gcc aaa ggc 882
 Phe Thr Ala His Asn Leu Val Lys Thr Leu Ser Arg Leu Ala Lys Gly
 250 255 260

aac cgg ctg gtg ctc atc tcc ctc cac cag cct cgc tct gac atc ttc 930
 Asn Arg Leu Val Leu Ile Ser Leu His Gln Pro Arg Ser Asp Ile Phe
 265 270 275

agg ctg ttt gat ctg gtc ctc ctg atg acg tct ggc acc ccc atc tac 978
 Arg Leu Phe Asp Leu Val Leu Leu Met Thr Ser Gly Thr Pro Ile Tyr
 280 285 290

tta ggg gcg gcc cag cac atg gtc cag tat ttc aca gcc atc ggc tac 1026
 Leu Gly Ala Ala Gln His Met Val Gln Tyr Phe Thr Ala Ile Gly Tyr
 295 300 305

ccc tgt cct cgc tac agc aat cct gct gac ttc tat gtg gac ctg acc 1074
 Pro Cys Pro Arg Tyr Ser Asn Pro Ala Asp Phe Tyr Val Asp Leu Thr
 310 315 320 325

agc att gac agg cgc agc aga gag cag gaa ttg gcc acc agg gag aag 1122
 Ser Ile Asp Arg Arg Ser Arg Glu Gln Glu Leu Ala Thr Arg Glu Lys
 330 335 340

gct cag tca ctc gca gcc ctg ttt cta gaa aaa gtg cgt gac tta gat 1170
 Ala Gln Ser Leu Ala Ala Leu Phe Leu Glu Lys Val Arg Asp Leu Asp
 345 350 355

gac ttt cta tgg aaa gca gag acg aag gat ctt gac gag gac acc tgt 1218
 Asp Phe Leu Trp Lys Ala Glu Thr Lys Asp Leu Asp Glu Asp Thr Cys
 360 365 370

gtg gaa agc agc gtg acc cca cta gac acc aac tgc ctc ccg agt cct 1266
 Val Glu Ser Ser Val Thr Pro Leu Asp Thr Asn Cys Leu Pro Ser Pro
 375 380 385

acg aag atg cct ggg gcg gtg cag cag ttt acg acg ctg atc cgt cgt 1314
 Thr Lys Met Pro Gly Ala Val Gln Gln Phe Thr Thr Leu Ile Arg Arg
 390 395 400 405

cag att tcc aac gac ttc cga gac ctg ccc acc ctc ctc atc cat ggg 1362
 Gln Ile Ser Asn Asp Phe Arg Asp Leu Pro Thr Leu Leu Ile His Gly
 410 415 420

gcg gag gcc tgt ctg atg tca atg acc atc ggc ttc ctc tat ttt ggc 1410
 Ala Glu Ala Cys Leu Met Ser Met Thr Ile Gly Phe Leu Tyr Phe Gly
 425 430 435

cat ggg agc atc cag ctc tcc ttc atg gat aca gcc gcc ctc ttg ttc 1458
 His Gly Ser Ile Gln Leu Ser Phe Met Asp Thr Ala Ala Leu Leu Phe
 440 445 450

atg atc ggt gct ctc atc cct ttc aac gtc att ctg gat gtc atc tcc 1506
 Met Ile Gly Ala Leu Ile Pro Phe Asn Val Ile Leu Asp Val Ile Ser
 455 460 465

aaa tgt tac tca gag agg gca atg ctt tac tat gaa ctg gaa gac ggg 1554
 Lys Cys Tyr Ser Glu Arg Ala Met Leu Tyr Tyr Glu Leu Glu Asp Gly
 470 475 480 485

ctg tac acc act ggt cca tat ttc ttt gcc aag atc ctc ggg gag ctt 1602
 Leu Tyr Thr Thr Gly Pro Tyr Phe Phe Ala Lys Ile Leu Gly Glu Leu
 490 495 500

ccg gag cac tgt gcc tac atc atc atc tac ggg atg ccc acc tac tgg 1650
 Pro Glu His Cys Ala Tyr Ile Ile Ile Tyr Gly Met Pro Thr Tyr Trp
 505 510 515

ctg gcc aac ctg agg cca ggc ctc cag ccc ttc ctg ctg cac ttc ctg 1698
 Leu Ala Asn Leu Arg Pro Gly Leu Gln Pro Phe Leu Leu His Phe Leu
 520 525 530

ctg gtg tgg ctg gtg gtc ttc tgt tgc agg att atg gcc ctg gcc gcc 1746
 Leu Val Trp Leu Val Val Phe Cys Cys Arg Ile Met Ala Leu Ala Ala
 535 540 545

gcg gcc ctg ctc ccc acc ttc cac atg gcc tcc ttc ttc agc aat gcc 1794
 Ala Ala Leu Leu Pro Thr Phe His Met Ala Ser Phe Phe Ser Asn Ala
 550 555 560 565

ctc tac aac tcc ttc tac ctc gcc ggg ggc ttc atg ata aac ttg agc 1842
 Leu Tyr Asn Ser Phe Tyr Leu Ala Gly Gly Phe Met Ile Asn Leu Ser
 570 575 580

agc ctg tgg aca gtg ccc gcg tgg att tcc aaa gtg tcc ttc ctg cgg 1890
 Ser Leu Trp Thr Val Pro Ala Trp Ile Ser Lys Val Ser Phe Leu Arg
 585 590 595

tgg tgt ttt gaa ggg ctg atg aag att cag ttc agc aga aga act tat 1938
 Trp Cys Phe Glu Gly Leu Met Lys Ile Gln Phe Ser Arg Arg Thr Tyr
 600 605 610

aaa atg cct ctc ggg aac ctc acc atc gcg gtc tca gga gat aaa atc 1986
 Lys Met Pro Leu Gly Asn Leu Thr Ile Ala Val Ser Gly Asp Lys Ile
 615 620 625

ctc agt gcc atg gag ctg gac tcg tac cct ctc tac gcc atc tac ctc 2034
 Leu Ser Ala Met Glu Leu Asp Ser Tyr Pro Leu Tyr Ala Ile Tyr Leu
 630 635 640 645

atc gtc att ggc ctc agc ggt ggc ttc atg gtc ctg tac tac gtg tcc 2082
 Ile Val Ile Gly Leu Ser Gly Gly Phe Met Val Leu Tyr Tyr Val Ser
 650 655 660

tta agg ttc atc aaa cag aaa cca agt caa gac tgg tga ttcacgccag 2131
 Leu Arg Phe Ile Lys Gln Lys Pro Ser Gln Asp Trp
 665 670

acgtctgccc gctggtgggg gacctgagca gacccttcaa ctgcactccc tcctcaggag 2191

cccccttctg gggacagtga ggacaatgac cctacagatg ctcagctaca tccggcccag 2251

ggtgctgcag tggcacagac cagccacagg atggcagtag aataaagaca gtcgaaaggg 2311

atttctgctc actggcagga gactgcatg actgggagaa aacctgcact cgggtggcacc 2371

tacaacgttg ctaatttatt tccttttgat atgcatttat ataggcaact cgatatagga 2431

tgggagcaaa ctaggaatga attgggtagc tagactgtgc aggaattgtt ggaacctgga 2491

gggaacaata acagtagcta gcagatttgg cttcatcttc caggggcccc acactccgtg 2551

gtgagccacc atcaatacag aaagtgacct aagatgtacc agcaagatgc catcccttct 2611

ttttgtgtgg ggtcatgggc tccaaaagcc aacgtgaaca attaaaaatg tattgagc 2669

<210> 8

<211> 673

<212> PRT

<213> Homo sapiens

<220>

<223> human ABCG8 (hABCG8)

<400> 8

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 Pro Gln Asp Thr Ser Gly Leu Gln Asp Arg Leu Phe Ser Ser Glu Ser
 20 25 30
 Asp Asn Ser Leu Tyr Phe Thr Tyr Ser Gly Gln Pro Asn Thr Leu Glu
 35 40 45
 Val Arg Asp Leu Asn Tyr Gln Val Asp Leu Ala Ser Gln Val Pro Trp
 50 55 60
 Phe Glu Gln Leu Ala Gln Phe Lys Met Pro Trp Thr Ser Pro Ser Cys
 65 70 75 80
 Gln Asn Ser Cys Glu Leu Gly Ile Gln Asn Leu Ser Phe Lys Val Arg
 85 90 95

B1

Ser Gly Gln Met Leu Ala Ile Ile Gly Ser Ser Gly Cys Gly Arg Ala
 100 105 110
 Ser Leu Leu Asp Val Ile Thr Gly Arg Gly His Gly Gly Lys Ile Lys
 115 120 125
 Ser Gly Gln Ile Trp Ile Asn Gly Gln Pro Ser Ser Pro Gln Leu Val
 130 135 140
 Arg Lys Cys Val Ala His Val Arg Gln His Asn Gln Leu Leu Pro Asn
 145 150 155 160
 Leu Thr Val Arg Glu Thr Leu Ala Phe Ile Ala Gln Met Arg Leu Pro
 165 170 175
 Arg Thr Phe Ser Gln Ala Gln Arg Asp Lys Arg Val Glu Asp Val Ile
 180 185 190
 Ala Glu Leu Arg Leu Arg Gln Cys Ala Asp Thr Arg Val Gly Asn Met
 195 200 205
 Tyr Val Arg Gly Leu Ser Gly Gly Glu Arg Arg Arg Val Ser Ile Gly
 210 215 220
 Val Gln Leu Leu Trp Asn Pro Gly Ile Leu Ile Leu Asp Glu Pro Thr
 225 230 235 240
 Ser Gly Leu Asp Ser Phe Thr Ala His Asn Leu Val Lys Thr Leu Ser
 245 250 255
 Arg Leu Ala Lys Gly Asn Arg Leu Val Leu Ile Ser Leu His Gln Pro
 260 265 270
 Arg Ser Asp Ile Phe Arg Leu Phe Asp Leu Val Leu Leu Met Thr Ser
 275 280 285
 Gly Thr Pro Ile Tyr Leu Gly Ala Ala Gln His Met Val Gln Tyr Phe
 290 295 300
 Thr Ala Ile Gly Tyr Pro Cys Pro Arg Tyr Ser Asn Pro Ala Asp Phe
 305 310 315 320
 Tyr Val Asp Leu Thr Ser Ile Asp Arg Arg Ser Arg Glu Gln Glu Leu
 325 330 335
 Ala Thr Arg Glu Lys Ala Gln Ser Leu Ala Ala Leu Phe Leu Glu Lys
 340 345 350
 Val Arg Asp Leu Asp Asp Phe Leu Trp Lys Ala Glu Thr Lys Asp Leu
 355 360 365
 Asp Glu Asp Thr Cys Val Glu Ser Ser Val Thr Pro Leu Asp Thr Asn
 370 375 380
 Cys Leu Pro Ser Pro Thr Lys Met Pro Gly Ala Val Gln Gln Phe Thr
 385 390 395 400
 Thr Leu Ile Arg Arg Gln Ile Ser Asn Asp Phe Arg Asp Leu Pro Thr
 405 410 415
 Leu Leu Ile His Gly Ala Glu Ala Cys Leu Met Ser Met Thr Ile Gly
 420 425 430
 Phe Leu Tyr Phe Gly His Gly Ser Ile Gln Leu Ser Phe Met Asp Thr
 435 440 445
 Ala Ala Leu Leu Phe Met Ile Gly Ala Leu Ile Pro Phe Asn Val Ile
 450 455 460
 Leu Asp Val Ile Ser Lys Cys Tyr Ser Glu Arg Ala Met Leu Tyr Tyr
 465 470 475 480
 Glu Leu Glu Asp Gly Leu Tyr Thr Thr Gly Pro Tyr Phe Phe Ala Lys
 485 490 495
 Ile Leu Gly Glu Leu Pro Glu His Cys Ala Tyr Ile Ile Ile Tyr Gly
 500 505 510
 Met Pro Thr Tyr Trp Leu Ala Asn Leu Arg Pro Gly Leu Gln Pro Phe
 515 520 525
 Leu Leu His Phe Leu Leu Val Trp Leu Val Val Phe Cys Cys Arg Ile
 530 535 540
 Met Ala Leu Ala Ala Ala Leu Leu Pro Thr Phe His Met Ala Ser
 545 550 555 560
 Phe Phe Ser Asn Ala Leu Tyr Asn Ser Phe Tyr Leu Ala Gly Gly Phe
 565 570 575

B1

Met Ile Asn Leu Ser Ser Leu Trp Thr Val Pro Ala Trp Ile Ser Lys
580 585 590
Val Ser Phe Leu Arg Trp Cys Phe Glu Gly Leu Met Lys Ile Gln Phe
595 600 605
Ser Arg Arg Thr Tyr Lys Met Pro Leu Gly Asn Leu Thr Ile Ala Val
610 615 620
Ser Gly Asp Lys Ile Leu Ser Ala Met Glu Leu Asp Ser Tyr Pro Leu
625 630 635 640
Tyr Ala Ile Tyr Leu Ile Val Ile Gly Leu Ser Gly Gly Phe Met Val
645 650 655
Leu Tyr Tyr Val Ser Leu Arg Phe Ile Lys Gln Lys Pro Ser Gln Asp
660 665 670
Trp

<210> 9
<211> 6043
<212> DNA
<213> Homo sapiens

<220>
<223> ABCG8 exon 2 (reverse strand) through ABCG5 exon 2
(forward strand)

B1

<400> 9
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agactgttgt cactttccga ggagaacaag ctgtcctgga ggccctgctg ggagacatgt 120
agtcaatgtg taagggtcac atgcagagag cgccttcccc gggttctcatt tctttgtgtt 180
ggaaaccatc agattcttct ctccgggtct tttgctttga aagtaaaatt tttattttat 240
tttgtgtgta tgactgtttg cctgcatgca tgtgcgtgcg ccacacacat acctggcacc 300
ctcagaggtc aaaagaggtc actgggtcct ctggacctgg agttatgggt ggttgtgaac 360
catctgtgtg tgatgggaat ggggtccagg tattctcagg tgcttttaat gtttgagcat 420
caccacagct ccattctctg atctttacta aaaaataata atagcaatgg cttaaactat 480
ggtcaccccg ctgtgcttca gaacactaga atttatgtct cccatctcat tttgatgcc 540
aggatctgac tgccaaccat cccctaccct gtaataataat tcatctctct gaagtaggaa 600
tatattggag atatcttttg ggggtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt 660
tggggaatca aatccatagc atcaaatata ctaggccaat catgatactg acagaaccat 720
agcaacacat ccgggggtccc tgggggtttct tgttttcaaa tcaattatct ttaggagaga 780
tcttagttac ttgcatgggc taggaatttg ttcttagaca cttgtactga tacaagttt 840
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 <211> 359
 <212> DNA
 <213> Homo sapiens

<220>
 <223> sequence between ABCG5 and ABCG8 containing
 control sequences (bidirectional promoter)

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<210> 11
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:6-His epitope
 tag

<400> 11
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 1 5

<210> 12
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:anti-DYKDDDDK
 epitope tag

<400> 12
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 1 5

<210> 13
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:flexible linker

<220>.
 <221> MOD_RES
 <222> (6)..(200)
 <223> Gly at positions 6-200 may be present or absent

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